

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT:
(A) NAME: Koninklijke Universiteit Nijmegen.
Afdeling tumorimmunologie
(B) STREET: Philips van Leydenlaan 25
(C) CITY: Nijmegen
10 (E) COUNTRY: Netherlands
(F) POSTAL CODE (ZIP): 6525 EX
(G) TELEPHONE: + 31 243 617 600
(H) TELEFAX: + 31 243 540 339
- 15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0. Version #1.30
- (ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING
DENDRITIC CELL-T CELL INTERACTION
- 25 (iii) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO:1:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | |
|----|---|-----|
| 45 | ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG | 60 |
| | AGAGGCCTTG GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT | 120 |
| | GGTCCCCTGG TGCTGCAACT CCTCTCCTTC ACGCTCTTGG CTGGGCTCCT TGTCCAAGTG | 180 |
| 50 | TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC | 240 |
| | CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC | 300 |
| 55 | TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG | 360 |

CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA 420
 TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT 480
 5 CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG 540
 GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CCGGCTGAAG 600
 10 GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC 660
 CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCAG 720
 GAGCTGACCC AGCTGAAGGC TGCAGTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG 780
 15 ACATTCTTCC AAGGAAACTG TTACTTCATG TCTAACTCCC AGCGGAACTG GCACGACTCC 840
 ATCACC GCCT GCAAAGAAGT GGGGGCCCAG CTCGTCGTAA TCAAAAGTGC TGAGGAGCAG 900
 20 AACTTCCTAC AGCTGCAGTC TTCCAGAAGT AACCGCTTCA CCTGGATGGG ACTTTCAGAT 960
 CTAAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG 1020
 CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT 1080
 25 GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC 1140
 GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTTCTTTCTC CAGCCCCTGC CACCCCAAAC 1200
 30 CCCCCTCCTG CGTAG 1215

2) INFORMATION FOR SEQ ID NO:2:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu
 1 5 10 15

Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly
 20 25 30

50

Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu
 35 40 45

55

Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val
 50 55 60

[illegible]

Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg
335 340 345

5 Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser
350 355 360

Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp
365 370 375

10 Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln
380 385 390

Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala *

15 395 400 404